

CRF Errors Edited by the STIC Systems
Branch

Serial Number: 10/622,377

CRF Edit Date: 7/28/89
Edited by: 262

___ Realigned nucleic acid/amino acid numbers/text in ~~ones~~ where the sequence
text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID
NO's edited:

___ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

✓ Other: deleted numbering under
stop codons in sequence # 9
and sequence #13.

Revised 09/09/2003



IFWO

RAW SEQUENCE LISTING

DATE: 08/05/2004

PATENT APPLICATION: US/10/622,377

TIME: 09:54:44

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\08042004\J622377.raw

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3 <110> APPLICANT: JENTSCH, THOMAS J.
5 <120> TITLE OF INVENTION: TEST SYSTEM FOR THE DEVELOPMENT OF THERAPEUTIC AGENTS,
6     IN PARTICULAR ACTIVE COMPOUNDS FOR THE TREATMENT OF
7     OSTEOPOROSIS
9 <130> FILE REFERENCE: 59572(46865)
11 <140> CURRENT APPLICATION NUMBER: 10/622,377
12 <141> CURRENT FILING DATE: 2003-07-18
14 <150> PRIOR APPLICATION NUMBER: PCT/DK02/00038
15 <151> PRIOR FILING DATE: 2002-01-17
17 <160> NUMBER OF SEQ ID NOS: 14
19 <170> SOFTWARE: PatentIn Ver. 3.2
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 3953
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: gene
28 <222> LOCATION: (1)..(3953)
29 <223> OTHER INFORMATION: CLCN3
31 <220> FEATURE:
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33 <222> LOCATION: (489)..(2951)
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51 aaaggcagcg caaaaaacag ccaccgattt tgctatgtct ctgagctgcg agataatcag 480
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55     1             5             10
57 agc tac aac agt ata aca agt gca agt agt gat gag gaa ctt tta gat 578
58 Ser Tyr Asn Ser Ile Thr Ser Ala Ser Ser Asp Glu Glu Leu Leu Asp
59 15             20             25             30
61 gga gca ggt gtt att atg gac ttt caa aca tct gaa gat gac aat tta 626
62 Gly Ala Gly Val Ile Met Asp Phe Gln Thr Ser Glu Asp Asp Asn Leu
63             35             40             45
65 tta gat ggt gac act gca gtt gga act cat tat aca atg aca aat gga 674
66 Leu Asp Gly Asp Thr Ala Val Gly Thr His Tyr Thr Met Thr Asn Gly

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Output Set: N:\CRF4\08042004\J622377.raw

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73 att cca ggt gtt ggt aca tat gat gat ttc cat act att gat tgg gtg 770
74 Ile Pro Gly Val Gly Thr Tyr Asp Asp Phe His Thr Ile Asp Trp Val
75          80          85          90
77 cga gaa aaa tgt aaa gac aga gaa agg cat aga cgg atc aac agc aaa 818
78 Arg Glu Lys Cys Lys Asp Arg Glu Arg His Arg Arg Ile Asn Ser Lys
79 95          100          105          110
81 aag aaa gaa tca gca tgg gaa atg aca aaa agt ttg tat gat gcg tgg 866
82 Lys Lys Glu Ser Ala Trp Glu Met Thr Lys Ser Leu Tyr Asp Ala Trp
83          115          120          125
85 tca gga tgg cta gta gta aca cta aca gga ttg gca tca ggg gca ctg 914
86 Ser Gly Trp Leu Val Val Thr Leu Thr Gly Leu Ala Ser Gly Ala Leu
87          130          135          140
89 gcc gga tta ata gac att gct gcc gat tgg atg act gac cta aag gag 962
90 Ala Gly Leu Ile Asp Ile Ala Ala Asp Trp Met Thr Asp Leu Lys Glu
91          145          150          155
93 ggc att tgc ctt agt gcg ttg tgg tac aac cac gaa cag tgc tgt tgg 1010
94 Gly Ile Cys Leu Ser Ala Leu Trp Tyr Asn His Glu Gln Cys Cys Trp
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97 gga tct aat gaa aca aca ttt gaa gag agg gat aaa tgt cca cag tgg 1058
98 Gly Ser Asn Glu Thr Thr Phe Glu Glu Arg Asp Lys Cys Pro Gln Trp
99 175          180          185          190
101 aaa aca tgg gca gaa tta atc ata ggt caa gca gag ggt cct ggt tct 1106
102 Lys Thr Trp Ala Glu Leu Ile Ile Gly Gln Ala Glu Gly Pro Gly Ser
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106 Tyr Ile Met Asn Tyr Ile Met Tyr Ile Phe Trp Ala Leu Ser Phe Ala
107          210          215          220
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110 Phe Leu Ala Val Ser Leu Val Lys Val Phe Ala Pro Tyr Ala Cys Gly
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113 tct gga att cca gag att aaa act att tta agt gga ttc atc atc aga 1250
114 Ser Gly Ile Pro Glu Ile Lys Thr Ile Leu Ser Gly Phe Ile Ile Arg
115          240          245          250
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118 Gly Tyr Leu Gly Lys Trp Thr Leu Met Ile Lys Thr Ile Thr Leu Val
119 255          260          265          270
121 ctg gct gtg gca tca ggt ttg agt tta gga aaa gaa ggt ccc ctg gta 1346
122 Leu Ala Val Ala Ser Gly Leu Ser Leu Gly Lys Glu Gly Pro Leu Val
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125 cat gtt gcc tgt tgc tgc gga aat atc ttt tcc tac ctc ttt cca aag 1394
126 His Val Ala Cys Cys Cys Gly Asn Ile Phe Ser Tyr Leu Phe Pro Lys
127          290          295          300
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130 Tyr Ser Thr Asn Glu Ala Lys Lys Arg Glu Val Leu Ser Ala Ala Ser
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135		320					325				330						
137	ttt	agc	ctg	gaa	gag	ggt	agc	tat	tat	ttt	cct	ctc	aaa	act	tta	tgg	1538
138	Phe	Ser	Leu	Glu	Glu	Val	Ser	Tyr	Tyr	Phe	Pro	Leu	Lys	Thr	Leu	Trp	
139	335					340					345					350	
141	aga	tca	ttt	ttt	gct	gct	tta	gtg	gct	gca	ttt	ggt	ttg	agg	tcc	atc	1586
142	Arg	Ser	Phe	Phe	Ala	Ala	Leu	Val	Ala	Ala	Phe	Val	Leu	Arg	Ser	Ile	
143					355					360						365	
145	aat	cca	ttt	ggg	aac	agc	cgt	ctg	gtc	ctt	ttt	tat	gtg	gag	tat	cat	1634
146	Asn	Pro	Phe	Gly	Asn	Ser	Arg	Leu	Val	Leu	Phe	Tyr	Val	Glu	Tyr	His	
147			370						375					380			
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161	gtc	att	att	ggt	gca	gcc	att	act	gct	gtg	ata	gcc	ttc	cct	aat	cca	1826
162	Val	Ile	Ile	Val	Ala	Ala	Ile	Thr	Ala	Val	Ile	Ala	Phe	Pro	Asn	Pro	
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165	tac	act	agg	cta	aac	acc	agt	gaa	ctg	atc	aaa	gag	ctt	ttt	aca	gac	1874
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174	Asn	Ala	Ser	Lys	Ile	Val	Asp	Asp	Ile	Pro	Asp	Arg	Pro	Ala	Gly	Ile	
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177	gga	gta	tat	tca	gct	ata	tgg	cag	tta	tgc	ctg	gca	ctc	ata	ttt	aaa	2018
178	Gly	Val	Tyr	Ser	Ala	Ile	Trp	Gln	Leu	Cys	Leu	Ala	Leu	Ile	Phe	Lys	
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181	atc	ata	atg	aca	gta	ttc	act	ttt	ggc	atc	aag	ggt	cca	tca	ggc	ttg	2066
182	Ile	Ile	Met	Thr	Val	Phe	Thr	Phe	Gly	Ile	Lys	Val	Pro	Ser	Gly	Leu	
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185	ttc	atc	ccc	agc	atg	gcc	att	gga	gcg	atc	gca	gga	agg	att	gtg	ggg	2114
186	Phe	Ile	Pro	Ser	Met	Ala	Ile	Gly	Ala	Ile	Ala	Gly	Arg	Ile	Val	Gly	
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189	att	gcg	gtg	gag	cag	ctt	gcc	tac	tat	cac	cac	gac	tgg	ttt	atc	ttt	2162
190	Ile	Ala	Val	Glu	Gln	Leu	Ala	Tyr	Tyr	His	His	Asp	Trp	Phe	Ile	Phe	
191			545					550					555				
193	aag	gag	tgg	tgt	gag	gtc	ggg	gct	gat	tgc	att	aca	cct	ggc	ctt	tat	2210
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Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\08042004\J622377.raw

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202 Val Ser Leu Val Val Ile Val Phe Glu Leu Thr Gly Gly Leu Glu Tyr
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205 att gtt ccc ctt atg gct gca gtc atg acc agt aaa tgg gtt gga gat 2354
206 Ile Val Pro Leu Met Ala Ala Val Met Thr Ser Lys Trp Val Gly Asp
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211                               625                               630                               635
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214 Tyr Pro Phe Leu Asp Ala Lys Glu Glu Phe Glu Phe Thr His Thr Thr
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219 655                               660                               665                               670
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225 aat gaa acc agc tac aat gga ttt cct gtc ata atg tca aaa gaa tct 2594
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227                               690                               695                               700
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231                               705                               710                               715
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251                               785                               790                               795
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254 Lys Lys Asp Ile Leu Arg His Met Ala Gln Thr Ala Asn Gln Asp Pro
255                               800                               805                               810
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258 Ala Ser Ile Met Phe Asn
259 815                               820
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263 ttttctctct ttacaaaaaa agaaaggaaa tataaaagcc gggtttttgc aacatggttt 3101

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DATE: 08/05/2004

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Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\08042004\J622377.raw

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275 tctgtttaat tcatgaattg tatagttaag cattaccttt ctacattcca gaagagcctt 3461
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283 cactaaatgc ttggaacagt acacatgcac cacaacaaag gctcatcaaa caggtaaagt 3701
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289 taatgtgacc ggggtcttatg caaattttct atttctaaaa ctactactat gatatacaag 3881
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296 <210> SEQ ID NO: 2

297 <211> LENGTH: 820

298 <212> TYPE: PRT

299 <213> ORGANISM: Homo sapiens

301 <400> SEQUENCE: 2

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309 35 40 45
311 Gly Asp Thr Ala Val Gly Thr His Tyr Thr Met Thr Asn Gly Gly Ser
312 50 55 60
314 Ile Asn Ser Ser Thr His Leu Leu Asp Leu Leu Asp Glu Pro Ile Pro
315 65 70 75 80
317 Gly Val Gly Thr Tyr Asp Asp Phe His Thr Ile Asp Trp Val Arg Glu
318 85 90 95
320 Lys Cys Lys Asp Arg Glu Arg His Arg Arg Ile Asn Ser Lys Lys Lys
321 100 105 110
323 Glu Ser Ala Trp Glu Met Thr Lys Ser Leu Tyr Asp Ala Trp Ser Gly
324 115 120 125
326 Trp Leu Val Val Thr Leu Thr Gly Leu Ala Ser Gly Ala Leu Ala Gly
327 130 135 140
329 Leu Ile Asp Ile Ala Ala Asp Trp Met Thr Asp Leu Lys Glu Gly Ile
330 145 150 155 160
332 Cys Leu Ser Ala Leu Trp Tyr Asn His Glu Gln Cys Cys Trp Gly Ser
333 165 170 175
335 Asn Glu Thr Thr Phe Glu Glu Arg Asp Lys Cys Pro Gln Trp Lys Thr
336 180 185 190
338 Trp Ala Glu Leu Ile Ile Gly Gln Ala Glu Gly Pro Gly Ser Tyr Ile
339 195 200 205
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/622,377

DATE: 08/05/2004

TIME: 09:54:45

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\08042004\J622377.raw



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/622,377

DATE: 07/28/2004

TIME: 16:23:17

Input Set : A:\57246865.app

Output Set: N:\CRF4\07282004\J622377.raw

3 <110> APPLICANT: JENTSCH, THOMAS J.
 5 <120> TITLE OF INVENTION: TEST SYSTEM FOR THE DEVELOPMENT OF THERAPEUTIC AGENTS,
 6 IN PARTICULAR ACTIVE COMPOUNDS FOR THE TREATMENT OF
 7 OSTEOPOROSIS
 9 <130> FILE REFERENCE: 59572(46865)
 11 <140> CURRENT APPLICATION NUMBER: 10/622,377
 12 <141> CURRENT FILING DATE: 2003-07-18
 14 <150> PRIOR APPLICATION NUMBER: PCT/DK02/00038
 15 <151> PRIOR FILING DATE: 2002-01-17
 17 <160> NUMBER OF SEQ ID NOS: 14
 19 <170> SOFTWARE: PatentIn Ver. 3.2
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 3953
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 28 <222> LOCATION: (1)..(3953)
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 49 ctttcttcgg tggagctccg agggtagcta ggttctaggt ttgaaacaga tgcagaatcc 420
 51 aaaggcagcg caaaaaacag ccaccgattt tgctatgtct ctgagctgcg agataatcag 480
 53 acagctaa atg gag tct gag cag ctg ttc cat aga ggc tac tat aga aac 530
 54 Met Glu Ser Glu Gln Leu Phe His Arg Gly Tyr Tyr Arg Asn
 55 1 5 10
 57 agc tac aac agt ata aca agt gca agt agt gat gag gaa ctt tta gat 578
 58 Ser Tyr Asn Ser Ile Thr Ser Ala Ser Ser Asp Glu Glu Leu Leu Asp
 59 15 20 25 30
 61 gga gca ggt gtt att atg gac ttt caa aca tct gaa gat gac aat ttä 626
 62 Gly Ala Gly Val Ile Met Asp Phe Gln Thr Ser Glu Asp Asp Asn Leu
 63 35 40 45
 65 tta gat ggt gac act gca gtt gga act cat tat aca atg aca aat gga 674
 66 Leu Asp Gly Asp Thr Ala Val Gly Thr His Tyr Thr Met Thr Asn Gly

Does Not Comply
Corrected Diskette Needed

(pages 6-8)

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71	65 70 75			
73	att cca ggt gtt ggt aca tat gat gat ttc cat act att gat tgg gtg	770		
74	Ile Pro Gly Val Gly Thr Tyr Asp Asp Phe His Thr Ile Asp Trp Val			
75	80 85 90			
77	cga gaa aaa tgt aaa gac aga gaa agg cat aga cgg atc aac agc aaa	818		
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82	Lys Lys Glu Ser Ala Trp Glu Met Thr Lys Ser Leu Tyr Asp Ala Trp			
83	115 120 125			
85	tca gga tgg cta gta gta aca cta aca gga ttg gca tca ggg gca ctg	914		
86	Ser Gly Trp Leu Val Val Thr Leu Thr Gly Leu Ala Ser Gly Ala Leu			
87	130 135 140			
89	gcc gga tta ata gac att gct gcc gat tgg atg act gac cta aag gag	962		
90	Ala Gly Leu Ile Asp Ile Ala Ala Asp Trp Met Thr Asp Leu Lys Glu			
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93	ggc att tgc ctt agt gcg ttg tgg tac aac cac gaa cag tgc tgt tgg	1010		
94	Gly Ile Cys Leu Ser Ala Leu Trp Tyr Asn His Glu Gln Cys Cys Trp			
95	160 165 170			
97	gga tct aat gaa aca aca ttt gaa gag agg gat aaa tgt cca cag tgg	1058		
98	Gly Ser Asn Glu Thr Thr Phe Glu Glu Arg Asp Lys Cys Pro Gln Trp			
99	175 180 185 190			
101	aaa aca tgg gca gaa tta atc ata ggt caa gca gag ggt cct ggt tct	1106		
102	Lys Thr Trp Ala Glu Leu Ile Ile Gly Gln Ala Glu Gly Pro Gly Ser			
103	195 200 205			
105	tat atc atg aac tac ata atg tac atc ttc tgg gcc ttg agt ttt gcc	1154		
106	Tyr Ile Met Asn Tyr Ile Met Tyr Ile Phe Trp Ala Leu Ser Phe Ala			
107	210 215 220			
109	ttt ctt gca gtt tcc ctg gta aag gta ttt gct cca tat gcc tgt ggc	1202		
110	Phe Leu Ala Val Ser Leu Val Lys Val Phe Ala Pro Tyr Ala Cys Gly			
111	225 230 235			
113	tct gga att cca gag att aaa act att tta agt gga ttc atc atc aga	1250		
114	Ser Gly Ile Pro Glu Ile Lys Thr Ile Leu Ser Gly Phe Ile Ile Arg			
115	240 245 250			
117	ggt tac ttg gga aaa tgg act tta atg att aaa acc atc aca tta gtc	1298		
118	Gly Tyr Leu Gly Lys Trp Thr Leu Met Ile Lys Thr Ile Thr Leu Val			
119	255 260 265 270			
121	ctg gct gtg gca tca ggt ttg agt tta gga aaa gaa ggt ccc ctg gta	1346		
122	Leu Ala Val Ala Ser Gly Leu Ser Leu Gly Lys Glu Gly Pro Leu Val			
123	275 280 285			
125	cat gtt gcc tgt tgc tgc gga aat atc ttt tcc tac ctc ttt cca aag	1394		
126	His Val Ala Cys Cys Cys Gly Asn Ile Phe Ser Tyr Leu Phe Pro Lys			
127	290 295 300			
129	tat agc aca aac gaa gct aaa aaa agg gag gtg cta tca gct gcc tca	1442		
130	Tyr Ser Thr Asn Glu Ala Lys Lys Arg Glu Val Leu Ser Ala Ala Ser			
131	305 310 315			

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133	gct	gca	ggg	gtt	tct	gta	gct	ttt	ggg	gca	cca	att	gga	gga	gtt	ctt	1490
134	Ala	Ala	Gly	Val	Ser	Val	Ala	Phe	Gly	Ala	Pro	Ile	Gly	Gly	Val	Leu	
135		320					325				330						
137	ttt	agc	ctg	gaa	gag	gtt	agc	tat	tat	ttt	cct	ctc	aaa	act	tta	tgg	1538
138	Phe	Ser	Leu	Glu	Glu	Val	Ser	Tyr	Tyr	Phe	Pro	Leu	Lys	Thr	Leu	Trp	
139	335					340					345					350	
141	aga	tca	ttt	ttt	gct	gct	tta	gtg	gct	gca	ttt	gtt	ttg	agg	tcc	atc	1586
142	Arg	Ser	Phe	Phe	Ala	Ala	Leu	Val	Ala	Ala	Phe	Val	Leu	Arg	Ser	Ile	
143					355					360					365		
145	aat	cca	ttt	ggg	aac	agc	cgt	ctg	gtc	ctt	ttt	tat	gtg	gag	tat	cat	1634
146	Asn	Pro	Phe	Gly	Asn	Ser	Arg	Leu	Val	Leu	Phe	Tyr	Val	Glu	Tyr	His	
147			370						375					380			
149	aca	cca	tgg	tac	ctt	ttt	gaa	ctg	ttt	cct	ttt	att	ctt	cta	ggg	gta	1682
150	Thr	Pro	Trp	Tyr	Leu	Phe	Glu	Leu	Phe	Pro	Phe	Ile	Leu	Leu	Gly	Val	
151			385						390					395			
153	ttt	gga	ggg	ctt	tgg	gga	gcc	ttt	ttc	att	agg	gca	aat	att	gcc	tgg	1730
154	Phe	Gly	Gly	Leu	Trp	Gly	Ala	Phe	Phe	Ile	Arg	Ala	Asn	Ile	Ala	Trp	
155		400					405					410					
157	tgt	cgt	cga	cgc	aag	tcc	acg	aaa	ttt	gga	aag	tat	ccc	gtt	ctg	gaa	1778
158	Cys	Arg	Arg	Arg	Lys	Ser	Thr	Lys	Phe	Gly	Lys	Tyr	Pro	Val	Leu	Glu	
159	415					420					425					430	
161	gtc	att	att	gtt	gca	gcc	att	act	gct	gtg	ata	gcc	ttc	cct	aat	cca	1826
162	Val	Ile	Ile	Val	Ala	Ala	Ile	Thr	Ala	Val	Ile	Ala	Phe	Pro	Asn	Pro	
163					435					440					445		
165	tac	act	agg	cta	aac	acc	agt	gaa	ctg	atc	aaa	gag	ctt	ttt	aca	gac	1874
166	Tyr	Thr	Arg	Leu	Asn	Thr	Ser	Glu	Leu	Ile	Lys	Glu	Leu	Phe	Thr	Asp	
167					450					455				460			
169	tgt	ggg	ccc	ctg	gaa	tcc	tct	tct	ctt	tgt	gac	tac	aga	aat	gac	atg	1922
170	Cys	Gly	Pro	Leu	Glu	Ser	Ser	Ser	Leu	Cys	Asp	Tyr	Arg	Asn	Asp	Met	
171			465						470					475			
173	aat	gcc	agt	aaa	att	gtc	gat	gac	att	cct	gat	cgt	cca	gca	ggc	att	1970
174	Asn	Ala	Ser	Lys	Ile	Val	Asp	Asp	Ile	Pro	Asp	Arg	Pro	Ala	Gly	Ile	
175		480					485					490					
177	gga	gta	tat	tca	gct	ata	tgg	cag	tta	tgc	ctg	gca	ctc	ata	ttt	aaa	2018
178	Gly	Val	Tyr	Ser	Ala	Ile	Trp	Gln	Leu	Cys	Leu	Ala	Leu	Ile	Phe	Lys	
179	495					500					505					510	
181	atc	ata	atg	aca	gta	ttc	act	ttt	ggc	atc	aag	gtt	cca	tca	ggc	ttg	2066
182	Ile	Ile	Met	Thr	Val	Phe	Thr	Phe	Gly	Ile	Lys	Val	Pro	Ser	Gly	Leu	
183					515					520					525		
185	ttc	atc	ccc	agc	atg	gcc	att	gga	gcg	atc	gca	gga	agg	att	gtg	ggg	2114
186	Phe	Ile	Pro	Ser	Met	Ala	Ile	Gly	Ala	Ile	Ala	Gly	Arg	Ile	Val	Gly	
187			530						535					540			
189	att	gcg	gtg	gag	cag	ctt	gcc	tac	tat	cac	cac	gac	tgg	ttt	atc	ttt	2162
190	Ile	Ala	Val	Glu	Gln	Leu	Ala	Tyr	Tyr	His	His	Asp	Trp	Phe	Ile	Phe	
191			545						550					555			
193	aag	gag	tgg	tgt	gag	gtc	ggg	gct	gat	tgc	att	aca	cct	ggc	ctt	tat	2210
194	Lys	Glu	Trp	Cys	Glu	Val	Gly	Ala	Asp	Cys	Ile	Thr	Pro	Gly	Leu	Tyr	
195		560					565					570					
197	gcc	atg	gtt	ggg	gct	gct	gca	tgc	tta	ggg	ggg	gtg	aca	aga	atg	act	2258

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198 Ala Met Val Gly Ala Ala Cys Leu Gly Gly Val Thr Arg Met Thr
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201 gtc tcc ctg gtg gtt att gtt ttt gag ctt act gga ggc ttg gaa tat 2306
202 Val Ser Leu Val Val Ile Val Phe Glu Leu Thr Gly Gly Leu Glu Tyr
203 595 600 605
205 att gtt ccc ctt atg gct gca gtc atg acc agt aaa tgg gtt gga gat 2354
206 Ile Val Pro Leu Met Ala Ala Val Met Thr Ser Lys Trp Val Gly Asp
207 610 615 620
209 gcc ttt ggc agg gaa ggc att tat gaa gca cac atc cga tta aat gga 2402
210 Ala Phe Gly Arg Glu Gly Ile Tyr Glu Ala His Ile Arg Leu Asn Gly
211 625 630 635
213 tac cct ttc ttg gat gca aaa gaa gaa ttc gaa ttc act cat acc acc 2450
214 Tyr Pro Phe Leu Asp Ala Lys Glu Glu Phe Glu Phe Thr His Thr Thr
215 640 645 650
217 ctg gct gct gac gtt atg aga cct cga agg aat gat cct ccc tta gct 2498
218 Leu Ala Ala Asp Val Met Arg Pro Arg Arg Asn Asp Pro Pro Leu Ala
219 655 660 665 670
221 gtc ctg aca cag gac aat atg aca gtg gat gat ata gaa aac atg att 2546
222 Val Leu Thr Gln Asp Asn Met Thr Val Asp Asp Ile Glu Asn Met Ile
223 675 680 685
225 aat gaa acc agc tac aat gga ttt cct gtc ata atg tca aaa gaa tct 2594
226 Asn Glu Thr Ser Tyr Asn Gly Phe Pro Val Ile Met Ser Lys Glu Ser
227 690 695 700
229 cag aga tta gtg gga ttt gcc ctc aga aga gac ctg aca att gca ata 2642
230 Gln Arg Leu Val Gly Phe Ala Leu Arg Arg Asp Leu Thr Ile Ala Ile
231 705 710 715
233 gaa agt gcc agg aaa aaa caa gaa ggt atc gtt ggc agt tct cgg gtg 2690
234 Glu Ser Ala Arg Lys Lys Gln Glu Gly Ile Val Gly Ser Ser Arg Val
235 720 725 730
237 tgt ttt gca cag cac acc cca tct ctt cca gca gaa agt cct cgg cca 2738
238 Cys Phe Ala Gln His Thr Pro Ser Leu Pro Ala Glu Ser Pro Arg Pro
239 735 740 745 750
241 ttg aag ctt cga agc att ctt gac atg agc cct ttt aca gtg aca gac 2786
242 Leu Lys Leu Arg Ser Ile Leu Asp Met Ser Pro Phe Thr Val Thr Asp
243 755 760 765
245 cac acc cca atg gag att gtg gtg gat att ttc cga aag ctg gga ctg 2834
246 His Thr Pro Met Glu Ile Val Val Asp Ile Phe Arg Lys Leu Gly Leu
247 770 775 780
249 agg cag tgc ctt gta act cac aat ggg cgc ctc ctt ggc att ata aca 2882
250 Arg Gln Cys Leu Val Thr His Asn Gly Arg Leu Leu Gly Ile Ile Thr
251 785 790 795
253 aaa aaa gat atc ctc cgg cat atg gcc cag acg gca aac caa gac ccc 2930
254 Lys Lys Asp Ile Leu Arg His Met Ala Gln Thr Ala Asn Gln Asp Pro
255 800 805 810
257 gct tca ata atg ttc aac tga atctcacaga tgaggagaga gaagaaacgg 2981
258 Ala Ser Ile Met Phe Asn
259 815 820
261 aagaggaagt ttatttggtt aatagcacia ctctttaacc tgagggagtc atctactttt 3041
263 ttttctcct ttacaaaaaa agaaaggaaa tataaaagcc ggggtttttgc aacatggttt 3101

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Input Set : A:\57246865.app

Output Set : N:\CRF4\07282004\J622377.raw

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265 gcaaataatg ctggtggaat ggaggagttg tttggggagg gaaaggagag agaaggaaag 3161
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269 atgcattcag ctgaggatgt gcctgatagt gcaggcttgc gcctcaacag agatgacagc 3281
271 agagtccctg agcacctggc ctgtttgctc acatgcaaga cacatacagc cctattctag 3341
273 aggatacttg aatggacctc tataaacgca aggttcttgc ctttttttaa tcaaaactgt 3401
275 tctgtttaat tcatgaattg tatagttaag cattaccttt ctacattcca gaagagcctt 3461
277 tattttctctc tctctctctc tctctctctc tctctctact gagctgtaac aaagcctctt 3521
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281 tgaggtttca tcacaagaag ggagtgtttc ttgtgccatt aaccatgtag tttgtaccat 3641
283 cactaaatgc ttggaacagt acacatgcac cacaacaaag gctcatcaaa caggtaaagt 3701
285 ctggaaggaa gcgagaacga aatctctcat tgtgtgccgt gtggctcaaa accgaaaaca 3761
287 atgaagcttg gttttaaagg ataaagtttt cttttttgtt ttctctcag actttatgga 3821
289 taatgtgacc gggctttatg caaattttct atttctaaaa ctactactat gatatacaag 3881
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296 <210> SEQ ID NO: 2

297 <211> LENGTH: 820

298 <212> TYPE: PRT

299 <213> ORGANISM: Homo sapiens

301 <400> SEQUENCE: 2

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306           20           25           30
308 Gly Val Ile Met Asp Phe Gln Thr Ser Glu Asp Asp Asn Leu Leu Asp
309           35           40           45
311 Gly Asp Thr Ala Val Gly Thr His Tyr Thr Met Thr Asn Gly Gly Ser
312           50           55           60
314 Ile Asn Ser Ser Thr His Leu Leu Asp Leu Leu Asp Glu Pro Ile Pro
315           65           70           75           80
317 Gly Val Gly Thr Tyr Asp Asp Phe His Thr Ile Asp Trp Val Arg Glu
318           85           90           95
320 Lys Cys Lys Asp Arg Glu Arg His Arg Arg Ile Asn Ser Lys Lys Lys
321           100          105          110
323 Glu Ser Ala Trp Glu Met Thr Lys Ser Leu Tyr Asp Ala Trp Ser Gly
324           115          120          125
326 Trp Leu Val Val Thr Leu Thr Gly Leu Ala Ser Gly Ala Leu Ala Gly
327           130          135          140
329 Leu Ile Asp Ile Ala Ala Asp Trp Met Thr Asp Leu Lys Glu Gly Ile
330          145          150          155          160
332 Cys Leu Ser Ala Leu Trp Tyr Asn His Glu Gln Cys Cys Trp Gly Ser
333           165          170          175
335 Asn Glu Thr Thr Phe Glu Glu Arg Asp Lys Cys Pro Gln Trp Lys Thr
336           180          185          190
338 Trp Ala Glu Leu Ile Ile Gly Gln Ala Glu Gly Pro Gly Ser Tyr Ile
339           195          200          205
341 Met Asn Tyr Ile Met Tyr Ile Phe Trp Ala Leu Ser Phe Ala Phe Leu
342           210          215          220
344 Ala Val Ser Leu Val Lys Val Phe Ala Pro Tyr Ala Cys Gly Ser Gly

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/622,377

DATE: 07/28/2004

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Input Set : A:\57246865.app

Output Set: N:\CRF4\07282004\J622377.raw

L:1779 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9

L:2648 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13

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<210> SEQ ID NO 14

Does Not Comply
Corrected Diskette Needed

Seq ID# 9 (PARTIAL sequence)

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ctg cag gcc cgg ctg agg cag cac tac cag acc atc tga cagcccagcc 2646
Leu Gln Ala Arg Leu Arg Gln His Tyr Gln Thr Ile
860 865

870
Delete